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MORGAN LEWIS & BOCKIUS LLP (WA)
1111 PENNSYLVANIA AVENUE NW
WASHINGTON, DC 20004

EXAMINER

ZOU, NIANXIANG

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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte YEE-PENG CHAN and CHRISTOPHER BRODER

Appeal 2016-000148¹
Application 12/808,930²
Technology Center 1600

Before DONALD E. ADAMS, DEMETRA J. MILLS, and
RYAN H. FLAX, *Administrative Patent Judges*.

ADAMS, *Administrative Patent Judge*.

DECISION ON APPEAL

This appeal under 35 U.S.C. § 134(a) involves claims 1, 5–7, 10–13, 15, and 19 (App. Br. 3).³ Examiner entered rejections under 35 U.S.C. § 101 and 35 U.S.C. § 103(a). We have jurisdiction under 35 U.S.C. § 6(b). We AFFIRM.

¹ The record includes a transcript of the oral hearing held October 12, 2017.

² Appellants identify the real party in interest as “The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc. (‘HJF’) and Zoetis, Inc.” (App. Br. 1.)

³ Pending “[c]laims 14, 16-18 and 20-25 . . . [stand] withdrawn from consideration” (App. Br. 3).

STATEMENT OF THE CASE

Appellants disclosure “relates[, *inter alia*,] to soluble forms of F glycoprotein from Hendra and Nipah viruses[] [and] to compositions comprising soluble forms of F glycoprotein from Hendra and Nipah virus” (Spec. ¶ 1). Claim 1 is representative and reproduced below:

1. A soluble polypeptide comprising a soluble antigenic form of a Nipah F glycoprotein, wherein the glycoprotein consists of an amino acid sequence with at least 90 percent sequence identity to amino acids 1 to 488 of SEQ ID NO: 4.

(App. Br. A-1.)

The claims stand rejected as follows:

Claims 1, 5–7, 15, and 19 stand rejected under 35 U.S.C. § 101 as directed to patent ineligible subject matter.

Claims 1, 5–7, 10, 11, 13, 15, and 19 stand rejected under 35 U.S.C. § 103(a) as unpatentable over the combination of Bossart-a,⁴ Bossart-b,⁵ Weingartl,⁶ and GenBank.⁷

⁴ Katharine N. Bossart et al., *Inhibition of Henipavirus fusion and infection by heptad-derived peptides of the Nipah virus fusion glycoprotein*, 2 VIROLOGY JOURNAL 1–15 (2005) (available at <http://www.virologyj.com/content/2/1/57>).

⁵ Katharine N. Bossart et al., *Receptor Binding, Fusion Inhibition, and Induction of Cross-Reactive Neutralizing Antibodies by a Soluble G glycoprotein of Hendra Virus*, 79 JOURNAL OF VIROLOGY 6690–6702 (2005).

⁶ Hana M. Weingartl et al., *Recombinant Nipah Virus Vaccines Protect Pigs against Challenge*, 80 JOURNAL OF VIROLOGY 7929–7938 (2006).

⁷ GenBank: CAD92362.1, accession number: CAD92362 (available at [http://www.ncbi.nlm.nih.gov/protein/40644716?report=genbank&log\\$=prot align&blast_rank=1&RID=G2GFMUSK01R](http://www.ncbi.nlm.nih.gov/protein/40644716?report=genbank&log$=prot%20align&blast_rank=1&RID=G2GFMUSK01R) (accessed Apr. 15, 2005)) (see Ans. 7). Appellants refer to this document as AbuBakar (see generally App. Br. 6).

Claim 12 stands rejected under 35 U.S.C. § 103(a) as unpatentable over the combination of Bossart-a, Bossart-b, Weingartl, GenBank, Weissenhorn,⁸ and Harbury.⁹

Obviousness:

ISSUE

Does the preponderance of evidence relied upon by Examiner support a conclusion of obviousness?

FACTUAL FINDINGS (FF)

FF 1. “Two novel zoonotic paramyxoviruses have emerged to cause disease in the past decade, Hendra virus (HeV) . . . , and Nipah virus (NiV)” (Bossart-a 2); *see* Bossart-b 6690 (Bossart-b discloses that “HeV and NiV are genetically closely related . . . and have been reclassified into the new *Henipavirus* genus”); *see generally* Ans. 8–9.

FF 2. “Paramyxoviruses contain two membrane-anchored glycoproteins that are required for virion attachment to and fusion with the membrane of the host cell” (Bossart-a 2; *see* Ans. 8).

FF 3. “The fusion protein (F) facilitates the fusion of virion and host cell membranes during virus infection, and is an oligomeric homotrimer” (Bossart-a 2; *see* Ans. 8).

FF 4. “GenBank[] . . . discloses the amino acid sequence of the F protein of Nipah virus showing that [] amino acid[s] 1-488 [of GenBank’s sequence

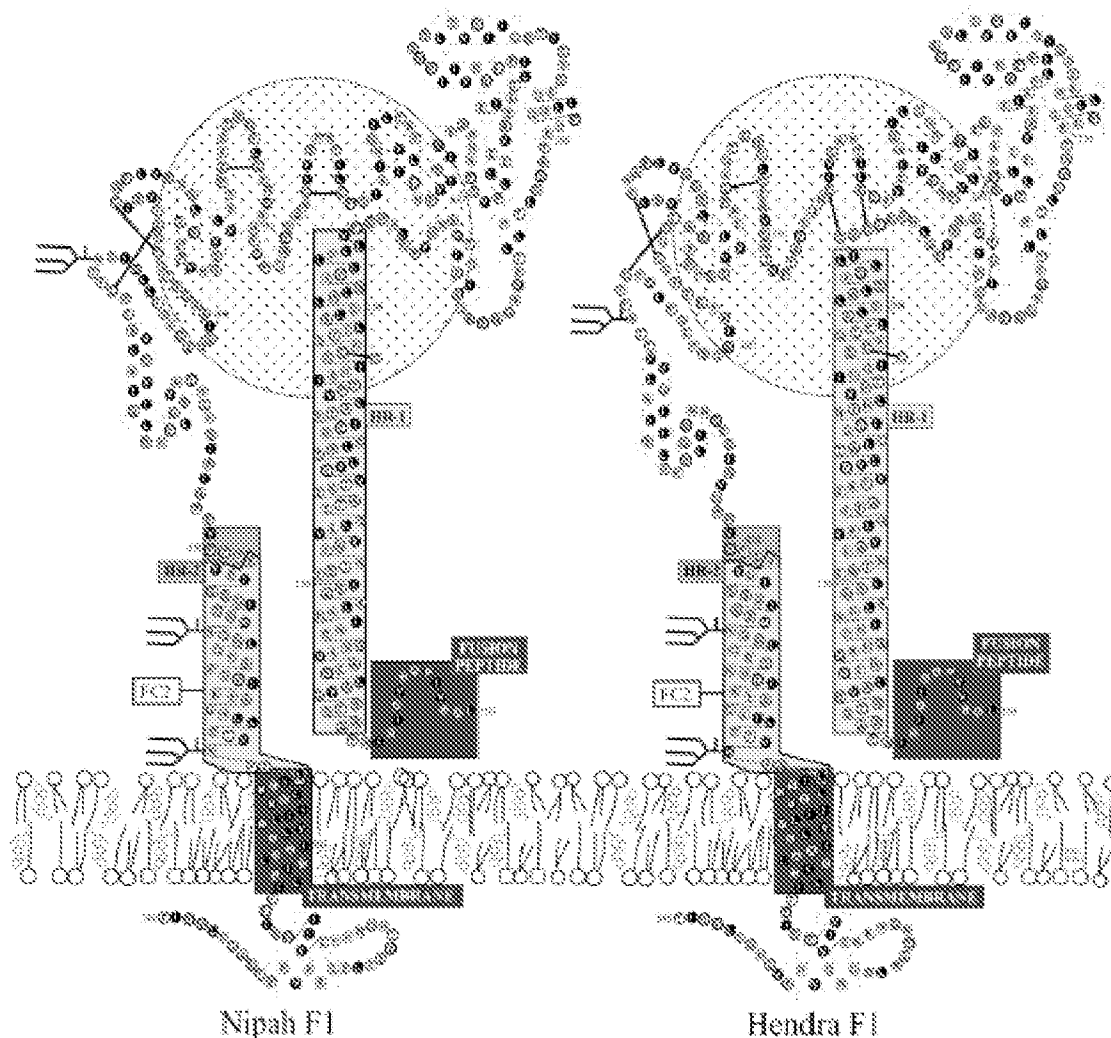
⁸ W. Weissenhorn et al., *Atomic structure of the ectodomain from HIV-1 gp41*, 387 NATURE 426–430 (1997).

⁹ Pehr B. Harbury et al., *Crystal structure of an isoleucine-zipper trimer*, 371 NATURE 80–83 (1994).

are] identical to [amino acids 1 to 488 of Appellants'] SEQ ID NO: 4" (Ans. 9; *see* Genbank).

FF 5. "The biologically active F protein consists of two disulfide linked subunits, F₁ and F₂, which are generated by the proteolytic cleavage of a precursor polypeptide known as F₀" (Bossart-a 2; Ans. 8 ("the biologically active F protein consists of two disulfide linked subunits, F₁ and F₂, which are generated by the proteolytic cleavage of a precursor polypeptide known as F₀"))).

FF 6. Bossart-a's Figure 1 is reproduced below:



Bossart-a's Figure 1 illustrates:

Hypothetical models of the transmembrane (F1) glycoproteins of Hendra virus and Nipah virus. . . . The heptad repeats are indicated as HR-1 (grey) and HR-2 (yellow/orange), transmembrane anchor (blue). The F₂ subunit is represented by the circle behind the F₁ subunit. The 36 amino acid fusion inhibitor peptide sequence used in [Bossart-a's] . . . study is designated as FC2 and is boxed (yellow). The equivalent location of FC2 in the HeV F1 subunit is shown for comparison.

(Bossart-a 4; *see* Ans. 8 (“Bossart-a teaches that the F1 protein is a transmembrane glycoprotein consisting of an extramembrane domain including amino acid residues 110-488 and a transmembrane domain including amino acid residues 489-510 and a cytoplasmic tail”); Ans. 8 (“the F0 protein, which contains both the F1 and F2 fragments before proteolytic cleavage, also contains the transmembrane domain including amino acid residues 489-510 and the cytoplasmic tail”); Ans. 9 (Bossart-a's Figure 1 “discloses only a portion of [the] amino acid sequence of the Nipha F protein in which the amino terminal 109 amino acids [illustrated in GenBank] are not depicted”); Ans. 9 (GenBank “discloses [the] N-terminal 109 amino acids that are not depicted in Bossart-a”).)

FF 7. Bossart-a discloses:

One important feature of many of the[] fusion glycoproteins are two α -helical domains referred to as heptad repeats (HR) that are involved in the formation of a trimer-of-hairpins structure. . . . HR-1 is located proximal to the amino (N)-terminal fusion peptide and HR-2 precedes the transmembrane domain near the carboxyl (C)-terminus.

(Bossart-a 2.)

FF 8. Bossart-a discloses that “[a]lthough both HR-1 and HR-2 derived peptides exhibited fusion inhibitory activity, the HR-2 peptide (residues 447–489) was more potent and more soluble” (Bossart-a 3).

FF 9. Examiner finds that “Bossart-a does not teach a soluble polypeptide comprising a soluble antigenic form of a Nipah F [glycoprotein] consisting of [an amino acid] sequence with at least 90% identity to [amino acids] 1-488 of SEQ ID NO: 4 . . . [or the] addition of a second polypeptide” (Ans. 8).

FF 10. Bossart-a discloses:

The HeV and NiV HR-2 peptides differed at three locations (amino acids 450, 479 and 480) with phenylalanine, arginine and leucine in NiV replaced by tyrosine, lysine and isoleucine in HeV. . . . These differences in the sequence of either peptide did not alter their homologous or heterologous inhibitory activity, suggesting that either peptide possessed potential therapeutic activity to both HeV and NiV.

(Bossart-a 3.)

FF 11. Bossart-b discloses that a transmembrane protein can be solubilized by deleting its transmembrane region (*see* Ans. 9 (citing Bossart-b 6691: left column ¶¶ 2, 4); *see also* Ans. 10 (Bossart-b discloses “an epitope tagged (S epitope and myc epitope) soluble G [glycoprotein]”)); *see generally* Bossart-b, Abstract).

FF 12. Weingartl discloses that “Nipah virus . . . human infections were linked to transmission of the virus from pigs. Consequently, a swine vaccine able to abolish virus shedding is of veterinary and human health interest.”

Thus, Weingartl prepared viral-based “vaccine vectors carrying the gene for NiV glycoprotein (ALVAC-G) or the fusion protein (ALVAC-F)” and found that “the combined ALVAC-F/G vaccine appears to be a very promising

vaccine candidate for swine” (Weingartl, Abstract; *see also id.* at 7935 (“High levels of antibodies were induced by all vaccines, with ALVAC-G and ALVAC-F/G inducing higher neutralizing titers than the ALVAC-F vaccine”); *see generally* Ans. 9).

FF 13. Examiner reasons that “[o]ne skilled in the art would readily expect that the portions [of] F protein exposed to serum antibodies are the extramembrane domains since the transmembrane domains and the cytoplasmic tails are not accessible to antibodies. . . . Therefore, Weingartl implies that the extracellular domain of [the] F protein is antigenic” (Ans. 9–10).

FF 14. Examiner finds that the combination of Bossart-a, Bossart-b, GenBank, and Weingartl does “not teach a trimerization domain set forth in [Appellants’] SEQ ID NO: 10” (Ans. 11).

FF 15. Examiner finds that Weissenhorn discloses an amino acid sequence that differs from Appellants’ “SEQ ID NO: 10 by two amino acids at the N-terminus (lacking the N-terminal [methionine and lysine] of SEQ ID NO: 10)” (Ans. 12).

FF 16. Examiner finds that Harbury discloses “an amino acid sequence . . . , which differs from [Appellants’] SEQ ID NO: 10 by having 2 additional [arginines] at both ends” (*id.*).

ANALYSIS

The rejection over the combination of Bossart-a, Bossart-b, Weingartl, and GenBank:

Based on the combination of Bossart-a, Bossart-b, Weingartl, and GenBank, Examiner concludes that, at the time Appellants’ invention was made, it would have been *prima facie* obvious to produce a soluble antigenic form of a Nipah F glycoprotein by removing, or truncating, the F protein

transmembrane region (Ans. 10). In this regard, Examiner reasons that a person of ordinary skill in this “art would [have] reasonably expect[ed] that deletion of the transmembrane and cytoplasmic portion of any transmembrane protein would result in a form that is not membrane anchored” (*id.*). We find no error in Examiner’s prima facie case of obviousness.

Claim 1:

Appellants contend that Bossart-a, Bossart-b, and Weingartl fail to teach amino acids 1–109 of the Nipah F glycoprotein (App. Br. 22; *see* Reply Br. 7). Appellants recognize, however, that GenBank discloses the “full length amino acid sequence of 546 amino acids for the immature F protein,” including amino acids 1–488, which are identical to Appellants’ SEQ ID NO: 4 (App. Br. 22; *see* FF 4, 6; Ans. 20). Nevertheless, although Appellants’ claimed invention does not require knowledge of the various Nipah F domains, Appellants’ contend that GenBank does not identify the various Nipah F glycoprotein domains (e.g., the transmembrane domain) (App. Br. 22.; *see also id.* at 24–25; Reply Br. 8). Therefore, Appellants’ contend that when GenBank is considered in isolation, GenBank “does not teach a polypeptide consisting of an amino acid sequence with at least 90 percent sequence identity to amino acids 1 to 488 of SEQ ID NO: 4” (App. Br. 22). We are not persuaded.

At the time of Appellants’ claimed invention, those of ordinary skill in this art would have recognized the various Nipah F glycoprotein domains contained in GenBank’s Nipah F glycoprotein amino acid sequence (*see* FF 5–8). Thus, notwithstanding Appellants’ contention to the contrary, the

combination of Bossart-a, Bossart-b, GenBank, and Weingartl make obvious Appellants' claim 1 (*see* FF 1–13).

Further, the combination of Bossart-a, Bossart-b, GenBank, and Weingartl make obvious a soluble polypeptide comprising a soluble antigenic form of a Nipah F glycoprotein (FF 1–13). In this regard, a person of ordinary skill in this art would have recognized that a soluble antigenic polypeptide of Nipah F glycoprotein would be obtained by, *inter alia*, removing the transmembrane domain of the Nipah F glycoprotein (*see generally* FF 11). As Bossart-a illustrates, the transmembrane region of Nipah F glycoprotein consists of amino acids 489–510. Thus, a person of ordinary skill in this art interested in obtaining a soluble or non-membrane bound form of Nipah F glycoprotein would have found it *prima facie* obvious to remove residues 489–510 of the Nipah F glycoprotein.

Therefore, when taken in combination, Bossart-a, Bossart-b, GenBank, and Weingartl suggest a soluble polypeptide comprising a soluble antigenic form of a Nipah F glycoprotein, wherein the glycoprotein consists of an amino acid sequence with at least 90 percent sequence identity to amino acids 1 to 488, i.e. Appellants' SEQ ID NO: 4, of Nipah F glycoprotein, as is required by Appellants' claim 1 (*see* App. Br. A-1). For the foregoing reasons we are not persuaded Appellants' contentions regarding "small peptides" (*see id.* at 26; Reply Br. 7, 8).

Appellants' claim 1, reproduced above, is not limited to a linear polypeptide having amino acids 1–488 of the Nipah F glycoprotein (*see* App. Br. A-1). In addition, the preponderance of evidence on this record makes clear that the extra-cellular portion of the Nipah F glycoprotein, which includes amino acids 1–488, is antigenic (*see* FF 12–13; Ans. 26, 27).

Therefore, we are not persuaded by Appellants' contention that "there is no indication in any of the cited references that a polypeptide with a linear amino acid sequence with at least 90 percent sequence identify to amino acids 1 to 488 of SEQ ID NO: 4 could be antigenic" (App. Br. 22).

Appellants' claim 1 does not require a particular degree of antigenicity, therefore, we are not persuaded by Appellants' contention that "Weingartl[] teaches that [the] full-length F glycoprotein construct is not as effective as the full-length G glycoprotein" (*id.*; *see also id.* at 27; *cf.* App. Br. A-1). Further, as Examiner explains, those of ordinary skill in this art, at the time of Appellants' claimed invention, would have recognized that the antigenic portion of Nipah F glycoprotein is the extracellular portion of the glycoprotein (FF 13; *see also* FF 12). We recognize, Appellants' contention that Examiner's rationale is "an unsupported leap of faith" (Reply Br. 9). Appellants', however, fail to provide persuasive evidence or argument to support a contrary position. Therefore, we are not persuaded by Appellants' contentions regarding full-length Nipah F glycoprotein (App. Br. 27).

Appellants' provide no persuasive evidence or argument to support a conclusion that a person of ordinary skill in this art would not have recognized that a membrane bound protein can be solubilized by removal of the transmembrane domain of the protein (*see* FF 6, 11; Ans. 20, 22; *cf.* App. Br. 22, 26–27; Reply Br. 9). *See KSR Int'l Co. v. Teleflex Inc.*, 550 U.S. 398, 416 (2007) ("The combination of familiar elements according to known methods is likely to be obvious when it does no more than yield predictable results"). Therefore, we are not persuaded by Appellants' contention that "Bossart-b has little, if any, bearing on the presently claimed invention," because it discusses solubilizing a membrane bound protein, which is other

than Nipah F glycoprotein, by removing the transmembrane portion of the protein (App. Br. 22; *see also id.* at 25 (contrasting the HeV G and NiV F glycoproteins); Reply Br. 7–8).

We are not persuaded by Appellants’ contention, which relies on unpublished data, that a soluble form of Nipah F glycoprotein may exhibit different reactivity to specific proteases than a naturally occurring membrane bound form of the same protein (*see* App. Br. 22–23 (citing Chan¹⁰ 11463–11464 (“Experiments with a variety of incubation periods, concentrations, and temperatures were carried out, and . . . cleavage of purified sF by cathepsin L resulted only in degradation of the protein preparations (data not shown)”))). To the contrary, we agree with Examiner’s assertion that those of ordinary skill in this art, at the time of Appellants’ claimed invention, would have recognized that transmembrane proteins may exhibit different susceptibility to proteolytic enzymes than membrane-bound forms of the same protein (*see generally*, Ans. 15; *see also* Bossart-a 3 (designing a Nipah F-based “HR-2 derived peptide[s] with changes aimed at improving their solubility and *in vivo* half-life when administered to animals”))).

For the foregoing reasons we are not persuaded by Appellants’ contention that the combination of Bossart-a, Bossart-b, GenBank, and Weingartl “individually or collectively [fail to] teach a polypeptide consisting of an amino acid sequence of SEQ ID NO: 4” (App. Br. 24).

¹⁰ Yee-Peng Chan et al., *Biochemical, Conformational, and Immunogenic Analysis of Soluble Trimeric Forms of Henipavirus Fusion Glycoproteins*, 86 JOURNAL OF VIROLOGY 11457–11471 (2012).

Claim 7:

Appellants' claim 7 depends from and further limits the polypeptide of Appellants' claim 1 to require that the Nipah F glycoprotein is fused to a second peptide (App. Br. A-1). Based on the combination of Bossart-a, Bossart-b, Weingartl, and GenBank, Examiner concludes that, at the time of Appellants' claimed invention, it would have been *prima facie* obvious to prepare an epitope tagged soluble antigenic form of Nipah F glycoprotein consisting of amino acids 1–488 of the Nipah F glycoprotein to facilitate purification of the fusion protein (Ans. 10; *see* FF 1–13). We find no error in Examiner's conclusion of obviousness.

Therefore, we are not persuaded by Appellants' contention that "Examiner does not address a 'second polypeptide' anywhere except in a separate rejection of claim 12" (App. Br. 28; *see* FF 11).

For the reasons set forth above, with respect to Appellants' claim 1, we are not persuaded by Appellants' contention that "none of the cited references teaches or suggests the first member [, i.e., the soluble polypeptide of Appellants' claim 1,] of the fusion protein construct" (App. Br. 23).

Claim 15:

Appellants' claim 15 is reproduced below:

15. A pharmaceutical composition comprising the soluble polypeptide of claim 1 and a pharmaceutically acceptable carrier.

(App. Br. A-1.)

For the reasons set forth above, with respect to Appellants' claim 1, we are not persuaded by Appellants' contention that "none of the cited

references teaches or suggest a polypeptide consisting of an amino acid sequence with at least 90 percent sequence identity to amino acids 1 to 488 of SEQ ID NO: 4” or that “a portion of F glycoprotein (of any size) could be antigenic or be useful in pharmaceutical compositions” (App. Br. 23, 28–29; *see* FF 1–13).

Weingartl discloses the use of HeV G protein, Nipah F protein, and the combination of HeV G and Nipah F proteins as a vaccine (FF 12). Thus, for the foregoing reasons and notwithstanding Appellants’ contentions to the contrary, a person of ordinary skill in this art would have reasonably expected success in formulating a soluble polypeptide comprising a soluble antigenic form of a Nipah F glycoprotein, wherein the glycoprotein consists of an amino acid sequence with at least 90 percent sequence identity to amino acids 1 to 488 of SEQ ID NO: 4 with a pharmaceutically acceptable carrier to prepare a pharmaceutical composition (*see* App. Br. A-1; *cf. id.* at 29). Appellants’ provide no persuasive evidence or argument to support their intimation that the soluble Nipah F glycoprotein suggested by the combination of Bossart-a, Bossart-b, GenBank, and Weingartl would not fold in a manner so as to elicit an antigenic response (*see id.* at 29).

For the foregoing reasons, we are not persuaded by Appellants’ contention that “Examiner appears to be asserting that creating pharmaceutical compositions with a soluble, antigenic F glycoprotein from NiV would be obvious because another transmembrane protein, unrelated to the subject peptide, has been successfully ‘solubilized’” (App. Br. 30).

The rejection over the combination of the Bossart-a, Bossart-b, Weingartl, GenBank, Weissenhorn, and Harbury:

Appellants' claim 12 depends ultimately from and further limits Appellants' claim 1 to require a trimerization domain that is SEQ ID NO: 10 (*see* App. Br. A-1).

Based on the combination of Bossart-a, Bossart-b, Weingartl, GenBank, Weissenhorn, and Harbury, Examiner concludes that, at the time Appellants' invention was made, it would have been *prima facie* obvious to fuse the peptides disclosed by either of Weissenhorn or Harbury to a soluble Nipah F glycoprotein in order to "form [soluble] trimers that mimic the native structure of the F [glycoprotein] on the viral membrane" (Ans. 12). We are not persuaded.

As Appellants' explain, Examiner failed to establish that Weissenhorn or Harbury suggest a protein that has the amino acid sequence of SEQ ID NO: 10 (*see* App. Br. 23). In this regard, we recognize that Examiner concedes that the peptides disclosed by Weissenhorn and Harbury differ from the sequence set forth in Appellants' SEQ ID NO: 10 (*see* FF 15; *cf.* App. Br. A-1).

CONCLUSION OF LAW

The preponderance of evidence relied upon by Examiner supports a conclusion of obviousness. The rejection of claims 1, 7, and 15 under 35 U.S.C. § 103(a) as unpatentable over the combination of Bossart-a, Bossart-b, Weingartl, and GenBank is affirmed. Claims 5, 6, and 19 are not separately argued and fall with claim 1. Claims 10, 11, and 13 are not separately argued and fall with claim 7.

The preponderance of evidence relied upon by Examiner fails to support a conclusion of obviousness. The rejection of claim 12 under 35 U.S.C. § 103(a) as unpatentable over the combination of Bossart-a, Bossart-b, Weingartl, GenBank, Weissenhorn, and Harbury is reversed.

Patent Eligible Subject Matter:

ISSUE

Does the evidence of record support Examiner's finding that Appellants' claimed invention is directed to patent ineligible subject matter?

FACTUAL FINDINGS (FF)

FF 17. Examiner finds that the soluble polypeptide set forth in Appellants' claim 1 comprises "a fragment of a Nipah F glycoprotein" and, thus, "exists in a naturally occurring protein (Nipah F glycoprotein)" (Ans. 6; *see* FF 1–13).

FF 18. Examiner finds that "the only structural difference between the natural product and the claimed product appears to be cleavage of a fragment of the native product" and "there is no indication of any marked structural changes between the claimed product and the natural product" (Ans. 6; *see* FF 1–13).

ANALYSIS

Examiner finds that Appellants' claim 1 is directed to patent ineligible subject matter (*see* Ans. 4, 7). We agree.

The soluble polypeptide of Appellants' claim 1 is a fragment of the naturally occurring Nipah F glycoprotein (*see* App. Br. A-1; *cf.* FF 4, 17). Specifically, Appellants' claimed polypeptide lacks the transmembrane and

intra-cellular portion, i.e., amino acids 489–510, of Nipah F glycoprotein (see App. Br. A-1; cf. FF 6).

Association for Molecular Pathology v. Myriad Genetics, Inc., 133 S.Ct. 2107 (2013), is controlling. In *Myriad*, the Court considered claims directed to isolated DNA encoding the BRCA1 polypeptide and fragments of at least 15 nucleotides of that DNA. *Id.* at 2113. The Court held that “Myriad did not create anything. To be sure, it found an important and useful gene, but separating that gene from its surrounding genetic material is not an act of invention.” *Id.* at 2117. “Myriad found the location of the BRCA1 and BRCA2 genes, but that discovery, by itself, does not render the BRCA genes ‘new . . . composition[s] of matter,’ § 101, that are patent eligible.” *Id.* “Nor are Myriad's claims saved by the fact that isolating DNA from the human genome severs chemical bonds and thereby creates a nonnaturally occurring molecule.” *Id.* at 2118.

Myriad’s rationale applies regardless of whether the naturally occurring product is a fragment of a gene or a protein. Thus, severing the chemical bond between amino acids 488 and 489 of Nipah F glycoprotein does not create a nonnaturally occurring molecule. *See Id.* For the foregoing reasons, we find that Appellants’ claimed soluble polypeptide represents a product of nature.

We recognize Appellants’ contention that “amino acids 1-26 of the naturally occurring full length Nipah virus make up the signal peptide and . . . [a]mino acid residues 27-109 of the naturally occurring full length F peptide sequence constitute the F₂ portion,” wherein both of these amino acid regions are post-translationally cleaved from the full length peptide sequence (App. Br. 9–10; Reply Br. 1–3). Appellants’, however, fail to

identify an evidentiary basis on this record to support a finding that these specific post-translational modifications result in a nascent Nipah virus F protein that does not comprise, for at least some time, amino acids 1–488 (*see* FF 4). *In re Pearson*, 494 F.2d 1399, 1405 (CCPA 1974) (“Attorney’s argument in a brief cannot take the place of evidence”). Thus, notwithstanding Appellants’ contention to the contrary, Appellants’ claim 1 is directed to a product of nature (*cf.* App. Br. 9; Reply Br. 1–2).

Alice Corp. Pty. Ltd. v. CLS Bank Int’l, 134 S. Ct. 2347, 2355 (2014) sets forth the following two-step analysis for determining patent eligibility under Section 101:

First, we determine whether the claims at issue are directed to one of those patent-ineligible concepts [e.g., a law of nature, natural phenomenon, or abstract idea]. If so, we then ask, what else is there in the claims before us? . . . We have described step two of this analysis as a search for an inventive concept—i.e., an element or combination of elements that is sufficient to ensure that the patent in practice amounts to significantly more than a patent upon the ineligible concept itself.

Id. (alterations, citations, and quotation marks omitted).

With respect to *Alice*’s first step, we find that Appellants’ claim 1 is directed to a product of nature. Therefore, we turn to *Alice*’s second step, the search for an inventive concept.

Appellants contend that the soluble polypeptide set forth in their claim 1 is soluble (*see* App. Br. 10; Reply Br. 5–6). However, as discussed above, those of ordinary skill in this art, at the time of Appellants’ claimed invention, would have recognized that the removal of the transmembrane and intra-cellular portion of Nipah F glycoprotein would have resulted in a soluble Nipah F glycoprotein (*see* FF 1–13, 17–18). Thus, solubilizing the Nipah F glycoprotein does not amount to significantly more than a patent

upon the ineligible concept itself. To the contrary, a person of ordinary skill in this art, at the time of Appellants' claimed invention, would have recognized that solubilizing a membrane bound protein is routine in this art (*see* FF 11).

Appellants further contend that the soluble polypeptide set forth in their claim 1 has "different characteristics as indicated in their susceptibility to enzymatic action" (App. Br. 11 (citing Chan); *see also* Reply Br. 3–5). However, as discussed above, those of ordinary skill in this art, at the time of Appellants' claimed invention, would have recognized that transmembrane proteins may exhibit different susceptibility to proteolytic enzymes than membrane-bound forms of the same protein (*see generally*, Ans. 15; *see also* Bossart-a 3 (designing a Nipah F-based "HR-2 derived peptide[s] with changes aimed at improving their solubility and *in vivo* half-life when administered to animals")). Thus, recognizing that a non-membrane bound form of Nipah F glycoprotein may exhibit a difference in enzymatic susceptibility relative to a membrane bound form of Nipah F glycoprotein does not amount to significantly more than a patent upon the ineligible concept itself.

For the foregoing reasons, we are not persuaded by Appellants' contentions that their claim 1 encompasses patent eligible subject matter.

CONCLUSION OF LAW

The evidence of record supports Examiner's finding that Appellants' claimed invention is directed to patent ineligible subject matter. The rejection of claim 1 under 35 U.S.C. § 101 as directed to patent ineligible subject matter is affirmed. Claims 5–7, 15, and 16 are not separately argued and fall with claim 1.

Appeal 2016-000148
Application 12/808,930

TIME PERIOD FOR RESPONSE

No time period for taking any subsequent action in connection with this appeal may be extended under 37 C.F.R. § 1.136(a).

AFFIRMED